Cell Viability (MTS) Assay Experiment Template

Structured Documentation for Cytotoxicity and Dose-Response Profiling — From Cell Seeding Through 4PL Curve Fit and EC50 Reporting

Applies to

- Academic and cell-biology research laboratories
- Biotechnology and pharmaceutical R&D groups
- Drug-discovery and cytotoxicity-screening teams
- Contract research organizations (CROs)

Relevant compliance & integrity frameworks

- **FDA 21 CFR Part 11** — Electronic records and signatures
- **GLP** — Good Laboratory Practice for preclinical documentation
- **Data integrity (ALCOA+)** — Attributable, contemporaneous, defensible records
- **NIH / NSF** — Reproducibility and data-management requirements

LabLynx, Inc.
3350 Riverwood Pkwy SE, Suite 1900, Atlanta, GA 30339
866.522.5969 | elabeln.com | info@lablynx.com

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1. Executive Summary

In cell-based screening, viability is decision data. The percent-viability read at each dose — and the EC50 or CC50 the dose-response yields — is what a project team uses to decide which compounds are cytotoxic, which are tolerated, and which advance. But a viability number is only as trustworthy as the seeding, the plate uniformity, the assay quality, and the curve fit behind it. A CC50 read from a plate with a poor Z′-factor or uncorrected edge effects is not a weak result — it is a meaningless one. A dose grid that misses the inflection point yields a number with no real precision. And when per-well absorbance lives scattered across plate-reader CSVs and individual Prism files, viability cannot be compared reliably across cell lines, compounds, and plates — which is the entire point of a cytotoxicity campaign.

The ELabELN Cell Viability (MTS) Assay Experiment Template solves this by providing a pre-built, fully structured screen record that loads from the template library in a single click. It ships with a 10-step MTS protocol, validated plate-layout references, pre-wired dose-response and Z′-factor fields, and typed inputs for cell line, seed density, compound, dose range, replicate count, treatment duration, MTS incubation time, A490 readings, blank-subtracted viability, Z′-factor, and EC50. The CellTiter MTS reagent, doxorubicin stock, and DMSO controls link to the ELabELN inventory, and the tamper-evident audit trail captures every plate layout, every absorbance reading, and every curve-fit calculation.

This white paper describes what the template contains, the cytotoxicity and dose-response use case it is designed to support, the upstream and downstream workflows it connects to, the benefits it delivers to the scientist, and how a laboratory can deploy it and begin running viability screens within days.

> **Key benefit**
> Labs that adopt the Cell Viability template stop rebuilding the plate map every screen and lose no well, replicate, or fit parameter between the plate reader and the analysis tool. Assay quality is gated by the Z′-factor, every EC50 carries its plate layout and fit parameters, and viability becomes queryable across cell lines and compounds — the structured, comparable foundation a real cytotoxicity campaign and defensible lead-compound provenance depend on.

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2. What Is an MTS Cell Viability Assay, and Why Does Documentation Matter?

2.1 The Technique

An MTS cell viability assay measures the metabolic activity of a cell population as a proxy for the number of viable cells. Cells are seeded into a microplate, treated with a compound across a range of concentrations — typically a serial dilution spanning several orders of magnitude — and incubated. Viable cells reduce the MTS tetrazolium reagent to a colored formazan product, and the absorbance at 490 nm is proportional to the number of metabolically active cells. Plotting blank-subtracted percent viability against the logarithm of concentration produces a sigmoidal dose-response curve, and fitting that curve with a four-parameter logistic (4PL) model yields the half-maximal effect concentration (EC50, or CC50 for cytotoxicity), together with the Hill slope, the top and bottom plateaus, and a goodness-of-fit (R^2).

A viability number is only meaningful if the plate that produced it was performing well, which is why screening relies on the Z′-factor — a statistical measure of the separation between the vehicle and full-kill controls on the plate. A Z′-factor above 0.5 indicates an excellent assay; below it, the controls overlap too much to trust any viability value from that plate. The result therefore depends on a chain: an appropriate seed density, a uniform plate free of edge artifacts, correct blank subtraction, enough replicates for precision, a passing Z′-factor, and a well-constrained 4PL fit. Weakness anywhere in that chain produces a viability value that looks authoritative and is not.

Because the EC50 is the number that advances or kills a compound and is compared across an entire panel of cell lines, **the plate layout, the per-well absorbance, the Z′-factor, and the 4PL fit parameters are what make a viability value trustworthy and comparable to the next compound — which is exactly why they must live in one structured, queryable record rather than a folder of plate-reader exports.**

2.2 The Documentation Problem

Recording viability screens across plate-reader files and individual analysis workbooks creates a set of interconnected risks:

- The plate map is rebuilt by hand each screen, so an inconsistent layout or seed density quietly makes viability values non-comparable across compounds and cell lines.
- Edge effects and seeding variance go unrecorded, so a plate artifact can distort a CC50 without leaving a trace.
- The Z′-factor is noted on a plate summary and easily overlooked, so a viability value from a failing plate can enter the dataset as if it were valid.
- Per-well A490, blank-subtracted viability, and normalized inhibition live in a CSV disconnected from the cell line, compound, and fit.
- The 4PL fit parameters (EC50, Hill slope, top, bottom, R^2) sit in a standalone Prism file, unlinked to the plate that produced them.
- Reagent and compound lots are not captured against the screen, so a shift in viability cannot be traced to an MTS or compound batch.

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- Prior screens of the same compound or cell line cannot be retrieved to compare, so the dose-response trend is assembled by hand from scattered files.

These are the gaps that make viability data hard to trust and compare, and they are the gaps this template was designed to close.

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3. Template Overview: What Ships with the Template

The ELabELN Cell Viability (MTS) Assay Experiment Template is a pre-populated experiment record available to all ELabELN subscribers directly from the template library. It ships configured for an MTS-based cytotoxicity screen of doxorubicin against HeLa cells in 96-well format, with a 10-step protocol covering cell seeding through 4-parameter-logistic curve fit and EC50 reporting. The default protocol assumes Promega CellTiter 96 AQueous One Solution (MTS with phenazine ethosulfate), 5,000 cells per well seeded 24 hours before treatment, a 9-point 3-fold doxorubicin dilution from 10 µM to 1.5 nM, a 24-hour treatment, a 4-hour MTS development, and absorbance read at 490 nm. Every section is editable — the configuration is a tested baseline, not a locked format.

3.1 Template Sections at a Glance

The template populates the existing ELabELN experiment sections your lab already works in. Your team edits a working baseline instead of rebuilding the plate map from scratch every screen.

Section	What it pre-populates
Main Text	Assay design, compound notes, and the expected dose-response range, authored in the TinyMCE rich-text editor and linked to the upstream cell culture.
Extra Fields	Eleven structured, typed fields grouped as Cells, Compound, and Readout & QC — cell line, seed density, compound, dose range, replicate count, treatment duration, MTS incubation time, A490, blank-subtracted viability, *Z′*-factor, and EC50. Typed values make dose-response parameters queryable across plates.
Steps	A 10-step workflow checklist covering cell seeding through curve-fit reporting. Each tick is timestamped to the audit trail, and the reader run is auto-logged.
Compounds	The CellTiter MTS reagent, doxorubicin stock, DMSO vehicle, and HeLa working stock pre-linked from the compound database, with lot numbers carried in automatically and working concentrations shown inline.
Links & Resources	Pre-wired to the lab’s MTS Viability SOP v1.4, the doxorubicin compound datasheet, and prior dose-response results for this compound.
Storage & Files	−20 °C compound and MTS reagent storage, plus labelled attachment slots for plate-reader CSV exports and 4PL fit XLSX workbooks.

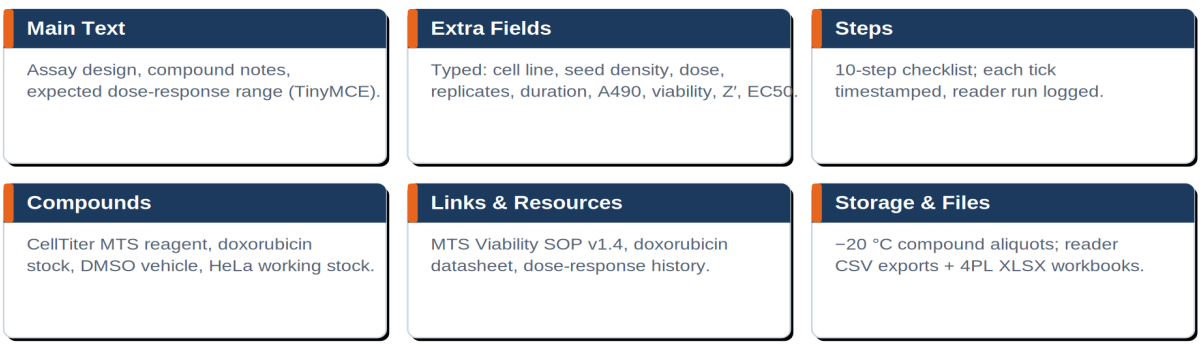
Main Text
Assay design, compound notes, expected dose-response range (TinyMCE).
Extra Fields
Typed: cell line, seed density, dose, replicates, duration, A490, viability, Z′, EC50.
Steps
10-step checklist; each tick timestamped, reader run logged.
Compounds
CellTiter MTS reagent, doxorubicin stock, DMSO vehicle, HeLa working stock.
Links & Resources
MTS Viability SOP v1.4, doxorubicin datasheet, dose-response history.
Storage & Files
−20 °C compound aliquots; reader CSV exports + 4PL XLSX workbooks.

Figure 1. The six ELabELN experiment sections pre-populated by the Cell Viability (MTS) template.

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3.2 The 10-Step Protocol

The workflow checklist is the operational spine of the template. Each step maps to a discrete bench or analysis action and writes a timestamped, user-attributed entry to the audit trail when checked off. The reader run is auto-logged, and the Z′-factor QC and 4PL curve fit are performed in the lab's analysis tool, with the resulting parameters recorded as typed fields.

Step	Action	What it captures
1	Seed HeLa cells (5,000/well)	Cell line; seed density; plate format
2	Prepare compound dilutions	High dose; dilution factor; dose points
3	Treat with doxorubicin (24 h)	Compound; dose range; treatment duration
4	Add MTS reagent	Detection reagent; volume
5	Develop (4 h, 37 °C)	MTS incubation time
6	Read absorbance (A490)	Per-well A490 (run auto-logged)
7	Blank-subtract	Blank A490; corrected signal
8	Normalize viability	% viability vs vehicle
9	Z′-factor QC	Z′-factor (external tool)
10	Fit 4PL / EC50	EC50, Hill slope, R² (external); e-signature

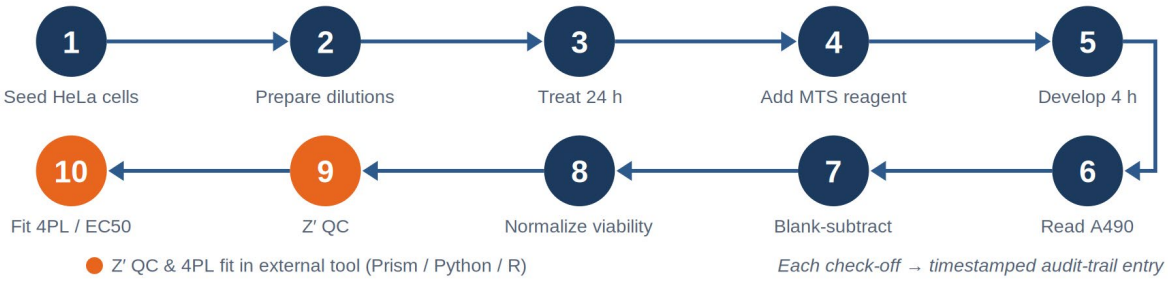

Figure 2. The 10-step MTS cell viability workflow — orange steps are the Z'-factor QC and 4PL curve fit performed in an external analysis tool (Prism / Python / R); every check-off writes a timestamped entry to the ELabELN audit trail.

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4. The Use Case: When and How the Template Is Used

The template is intended as a tested baseline for academic, biotechnology, and pharmacology research labs running viability and cytotoxicity work. It is configured around a recognizable reference — a doxorubicin-versus-HeLa MTS screen — but the scenarios it serves span the cytotoxicity bench and the discovery campaign it feeds.

4.1 Cytotoxicity and Dose-Response Profiling (Primary Use Case)

The core scenario: measuring how a compound affects cell viability across a dose range. The template captures the plate map, every replicate well, the Z′-factor, and the 4PL fit in one structured record, so an EC50 is fully reconstructable — which doses, which cell line, which assay quality, which fit — rather than a number in a spreadsheet detached from the plate that produced it.

4.2 Compound Screening and Hit Triage

Early screening asks a simple question: which compounds kill cells, and at what concentration. Because each screen's parameters are structured and queryable, toxic hits and tolerated compounds are triaged directly from the records rather than reconstructed from scattered files, and each result is linked to the plate and controls that justify it.

4.3 Selectivity and Therapeutic-Window Assessment

A compound's value often lies in the gap between the concentration that produces the intended effect and the concentration that becomes generally cytotoxic. Because viability EC50/CC50 values are typed and comparable to on-target potency, the template makes selectivity-window and therapeutic-index assessment straightforward rather than a manual cross-file exercise.

4.4 Cross-Cell-Line Potency Comparison

Cytotoxicity is frequently profiled across a panel of cell lines. Because every screen carries the same structured plate layout, seed density, and Z′-factor, the template makes the cross-line comparison at the heart of a selectivity or resistance study reliable rather than approximate.

4.5 Assay-Quality and Viability QC

Because EC50, Hill slope, and Z′-factor are typed and queryable, the template doubles as a running viability-QC record. A team can pull every screen of a compound or a cell line, compare potencies and assay quality side by side, and flag a plate whose Z′-factor undermines its result — before a questionable CC50 drives a decision.

4.6 Multi-Site and CRO Collaboration

Viability work is often split across sites and partners. Because every ELabELN edition includes unlimited users, the PI, scientists, and external collaborators can all work from the same records. Granular permissions let project leads control who can edit assay runs versus only review them — important during the multi-site CRO collaborations that discovery campaigns frequently involve.

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5. Dependencies and Connected Workflows

The Cell Viability template does not exist in isolation. It sits inside a network of connected workflows — upstream, parallel, external, and downstream — that give the screen record its full scientific and decision-making value.

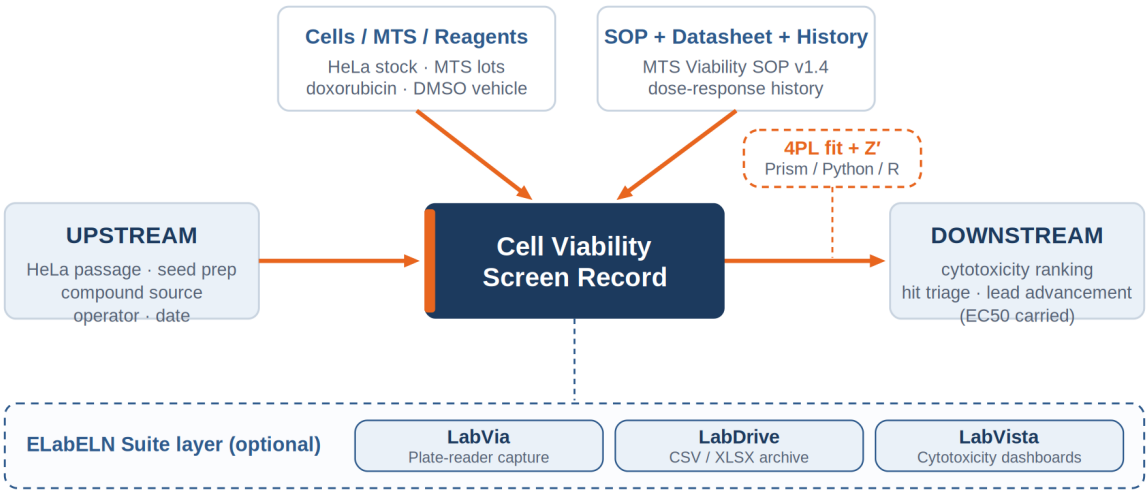

Figure 3. The template connects an upstream cell culture and compound source, parallel inventory and SOP/datasheet/history systems, the external plate reader and curve-fit tool, and downstream cytotoxicity-ranking, selectivity, and advancement workflows.

5.1 Upstream: Cell Culture and Compound Preparation

Every viability screen begins with a cultured cell line and a dose dilution prepared from a compound stock. The template links to the upstream cell passage and the dilution preparation, so opening a screen surfaces the cell line, its passage and seeding, the compound source, the operator, and the date — connecting each viability value to the culture and material that produced it.

5.2 Parallel: MTS Reagent, Compound, and Control Inventory

The Compounds section links the CellTiter MTS reagent, the doxorubicin stock, the DMSO vehicle, and the HeLa working stock directly to the ELabELN inventory. Because reagent identity and condition bear on the viability read, this traceability is decisive. Through the link the record automatically carries:

- **Lot numbers and aliquot tracking** for the MTS reagent and compounds, so a shift in viability can be traced to a reagent batch.
- **Working concentrations, shown inline**, so the exact assay conditions are on the record and reproducible.
- **Expiry and stock levels**, with low-stock warnings before a run, so a screen is not started against a depleted or expired reagent.

Barcode and QR scanning can populate these links from the physical vial, keeping lot capture effortless across a dose plate.

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5.3 Parallel: SOPs, the Compound Datasheet, and the Dose-Response History

The Links section connects the screen to the lab's MTS Viability SOP, the doxorubicin datasheet, and prior dose-response results for the compound. That last link is what turns individual screens into a campaign: each new EC50 opens alongside the dose-response history it belongs to, so the trend is built in rather than reconstructed.

5.4 External: The Plate Reader and Curve-Fit Tool

The plate reader produces the raw absorbance, and the 4PL curve fitting is performed in the lab's preferred analysis tool — GraphPad Prism, Python, or R. ELabELN is the system of record around that analysis: the full 8×12 well matrix (dose, well, A490, blank-subtracted viability) lives in the spreadsheet editor, ready for direct ingestion into the fitting tool, and the fit parameters (EC50, Hill slope, top, bottom, R^2) and the Z′-factor are written back into the typed Readout & QC fields, with the CSV and XLSX workbook attached. The plate data, the evidence, and the fitted EC50 stay together in one record.

5.5 Downstream: Cytotoxicity Ranking, Selectivity, and Advancement

The EC50 feeds cytotoxicity ranking, selectivity and therapeutic-window assessment, compound triage, and advancement calls, and — because viability and fit quality are typed and queryable — cross-compound and cross-line comparison. A compound-advancement decision rests on a documented, comparable viability profile rather than a number pulled from a standalone file.

5.6 The ELabELN Suite: Instruments and Dashboards

Everything above is available in ELabELN Standard. Labs on the ELabELN Suite gain three layers that connect to the same record: LabVia captures absorbance data directly from the plate reader; LabDrive adds metadata search, versioning, and role-based access across CSV and XLSX-workbook archives; and LabVista builds cross-plate cytotoxicity and dose-response dashboards on the structured viability metadata. The same audit trail and data-integrity controls span all layers.

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6. How the Scientist Benefits

The template is built to deliver value at the bench and to the campaign alike. The benefits compound with every screen a lab runs.

6.1 Start From a Tested Baseline, Not a Blank Plate Map

The scaffold — protocol, typed fields, plate map, reagent links, SOP, and dose-response history link — is already built. The scientist edits a working configuration to match the cell line and compound they actually screen, rather than rebuilding the plate map from scratch every time. The first screen is faster, and every subsequent one is consistent and comparable.

6.2 Document by Doing

Checking off each of the 10 steps as it happens produces a contemporaneous, timestamped record as a by-product of the screen, and the reader run is auto-logged. There is no separate write-up to reconstruct later.

6.3 Never Lose Plate-Map or Parameter Provenance Again

Because the plate map is a structured artifact and the reagents are linked to inventory, the layout, seed density, reagent lots, and fit parameters are captured permanently on every screen. When a viability value is questioned, the plate and its provenance are on the record — closing the most common cytotoxicity troubleshooting gap by default.

6.4 Cross-Cell-Line Viability You Can Query

Typed EC50, Hill-slope, and Z′-factor fields make the campaign queryable. A team can pull every screen of a compound or a cell line, trend viability compound by compound, and gate on assay quality at a glance — turning a folder of Prism files into a live dose-response view.

6.5 Assay-Quality Gating and Defensible Advancement

Capturing the Z′-factor beside every EC50 makes assay quality a visible, queryable gate rather than an afterthought, and the tamper-evident audit trail, reagent traceability, and electronic signatures give each advanced compound a defensible provenance — structured to support FDA 21 CFR Part 11 review and GLP-relevant preclinical documentation when the lab's quality system requires it.

> **At the bench, in practice**
>
> A scientist opens the template, sets the cell line and compound to match today's screen, scans the MTS reagent and compound vials to capture their lots, and checks off each step as the plate is seeded, treated, developed, and read. The reader absorbance populates the plate matrix; the data are fit in Prism, and the EC50, Hill slope, R^2, and Z′-factor go into typed fields — the Z′ confirming the plate was worth trusting. Weeks later, comparing the panel, the project lead queries every screen on that cell line and watches the CC50 shift across compounds, plate by validated plate.

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7. The Viability Plate and Assay Quality

7.1 The Default Reference: A Doxorubicin–HeLa MTS Screen

The template ships configured for an MTS cytotoxicity screen of doxorubicin against HeLa cells: 5,000 cells per well seeded 24 hours before treatment, a 9-point 3-fold dilution from 10 µM to 1.5 nM, a 24-hour treatment, a 4-hour MTS development, and absorbance read at 490 nm. Viability is normalized against on-plate vehicle and full-kill controls, the Z′-factor confirms the controls are well separated, and a 4PL fit returns the EC50 at half-maximal viability along with the Hill slope and goodness-of-fit. This concrete reference demonstrates the full seed-to-decision workflow out of the box; swap the cell line, readout reagent, or dose range to match what your lab screens.

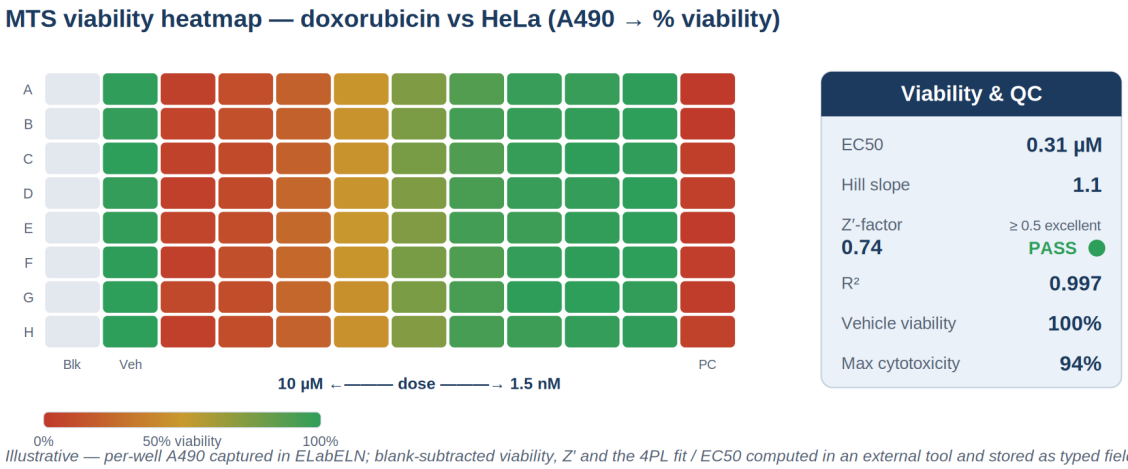

Figure 4. An 8×12 MTS viability heatmap across the dose plate, alongside the viability and assay-quality panel (with the Z'-factor gating validity). Illustrative; the per-well A490 is captured in ELabELN, and the 4PL fit is performed in an external tool with its parameters recorded as typed fields.

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7.2 How the Template Handles the Plate, Fit, and Z′-Factor

The full 8×12 well matrix — dose, well, A490, and blank-subtracted viability — lives in the spreadsheet editor, structured for direct ingestion into the fitting tool. Curve fitting itself is performed in GraphPad Prism, Python, or R, and the 4PL fit parameters (EC50, Hill slope, top, bottom, R^2) and the Z′-factor are written back into the typed Readout & QC fields, with the CSV and XLSX workbook attached. Because these values are structured and queryable, cross-screen comparison is straightforward: query every screen of a compound or cell line, gate on Z′-factor, and review EC50 and Hill slope side by side — the dose-response view a campaign runs on.

Element	Default configuration	Editable to
Cell line	HeLa (cervical carcinoma)	MCF7, A549, HCT116, primary cultures
Readout / reagent	MTS (CellTiter 96 AQ), A490	AlamarBlue, CellTiter-Glo (luminescent), trypan blue exclusion
Compound	Doxorubicin	Any small molecule, biologic, or natural product
Dose scheme	9-point 3-fold, 10 µM–1.5 nM	Any range, spacing, and replicate count
Format	96-well, 5,000 cells/well	384-well; any seed density / replicate scheme
Fit / endpoint	4PL, EC50 (cytotoxicity)	IC50; other models

Figure 5. The template's default configuration — fully editable for any cell line, readout reagent, dose scheme, or endpoint.

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8. Configuring the Template for Your Screen

Adapting the template to a different cell line or readout is a matter of editing the relevant sections — not rebuilding the structure.

8.1 Swap the Cell Line

Change the cell line — HeLa, MCF7, A549, HCT116, or a primary culture — by editing the Cells section, and adjust the seed density to match each line's growth rate. If the reagents already exist in the ELabELN compound database, simply re-link them; their lots and working concentrations flow in automatically.

8.2 Change the Readout Reagent

Switch the readout from MTS to AlamarBlue, CellTiter-Glo (luminescent), or trypan blue exclusion by editing the Readout section. The plate matrix and 4PL fit fields apply regardless of detection chemistry — only the raw signal type changes.

8.3 Adjust the Dose Scheme, Seed Density, and IC50 vs. EC50

Change the dose range, spacing, and replicate count to bracket your compound's activity, tune the seed density to the cell line, and move between EC50 and IC50 reporting by editing the curve-fit section. The 4PL model accommodates both.

8.4 Save a Custom Version

Once configured, save your edits as a private template scoped to your lab, or publish back to the ELabELN template library. Every subsequent screen opens from your configured baseline, and separate versions can be maintained for different cell lines, readout reagents, or plate formats.

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9. Getting Started

ELabELN Standard is a cloud-hosted SaaS deployment typically live within one to two business days of account creation. There is no hardware to buy, no IT project, and no per-seat licensing.

1. **Start an ELabELN account.** Visit elabeln.com/get-started. ELabELN Standard runs on LabLynx's managed cloud infrastructure.
2. **Provision your instance.** LabLynx provisions the instance within one to two business days; you receive a URL, admin credentials, and onboarding documentation.
3. **Load the Cell Viability template.** From the template library, select the Cell Viability (MTS) template and click "Use This Template." An editable instance opens immediately.
4. **Add your cells, reagents, and compounds to the inventory.** Enter your cell line and working stock, the MTS reagent, compounds, and DMSO controls with lot numbers and −20 °C storage locations. This is a one-time setup step.
5. **Link your SOP, datasheet, and dose-response history.** Upload your MTS Viability SOP and compound datasheet, and connect the compound's prior dose-response results to the template's Links section.
6. **Customize the template for your screen.** Edit the cell line, seed density, readout reagent, dose range, and replicate count, then save as a private team version.
7. **Run your first screen.** Open your saved template, complete the 10-step checklist, capture the plate matrix, record the Z′-factor and 4PL parameters, attach the CSV and XLSX workbook, and sign off.

> **Typical timeline**
> Day 1: Account requested at elabeln.com/get-started. Day 2–3: Instance provisioned; cell-line, reagent, and compound inventory populated; SOP, datasheet, and dose-response history linked. Day 3–4: Template configured and saved as a private version for your cell line and readout. Day 4–5: First screen documented in ELabELN with the plate matrix, Z′-factor, and EC50 captured and an e-signature.

9.1 ELabELN Standard vs. ELabELN Suite

Capability	Standard	Suite
Cell Viability template access	Included	Included
Unlimited users	Included	Included
Audit trail and e-signatures	Included	Included
Cell / reagent / compound inventory with lot tracking	Included	Included
SOP, datasheet & dose-response linking	Included	Included
Plate matrix + CSV / XLSX workbook attachments	Included	Included
LabVia direct plate-reader capture	—	Suite layer
LabDrive CSV / workbook archive search & versioning	—	Suite layer
LabVista cross-plate cytotoxicity & viability dashboards	—	Suite layer

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10. Frequently Asked Questions

Can I configure the template for my cell line and compound?

Yes. Every section is editable. Swap in any cell line (HeLa, MCF7, A549, HCT116, primary cultures), change the compound class (small molecule, biologic, natural product), adjust the dose range and replicate count, change the seed density per the line's growth rate, or move from MTS to AlamarBlue, CellTiter-Glo (luminescent), or trypan blue exclusion. Save your edits as a private template scoped to your lab, or publish back to the ELabELN template library.

Does the template calculate EC50 / IC50 automatically?

The template captures structured per-well absorbance, blank-subtracted viability, and the Z′-factor. Curve fitting (4-parameter logistic) is performed in your downstream analysis tool (GraphPad Prism, Python, R), then the EC50/IC50 value, slope, and R^2 are written back into the typed Readout & QC fields for queryable cross-experiment comparison. The spreadsheet editor captures the raw matrix that feeds the curve fit.

How does the template differ from the IC50 / Dose-Response template?

This template focuses on viability as the readout for cytotoxicity or basic cell health, with MTS, AlamarBlue, and CellTiter-Glo as common reagents. The IC50 / Dose-Response template focuses on the broader dose-response analysis framework that applies to enzyme inhibition, receptor binding, functional readouts, or viability — wherever you need EC50/IC50 extraction. Both share the dose-titration pattern but target different scientific questions.

Is it included in every ELabELN plan?

Yes. Every published template in the ELabELN library is available to all subscribers in both the Standard and Suite editions, with unlimited users in either edition and no per-template fee.

Can my whole lab use this template?

Yes. Every ELabELN edition includes unlimited users, so the PI, postdocs, grad students, rotating researchers, and visiting collaborators can all use the template without per-seat charges. Granular permissions let the PI control who can edit assay runs versus only review them.

How quickly can my lab start running viability assays in ELabELN?

ELabELN Standard cloud deployment is typically live in one to two business days. Once the instance is provisioned, the template loads from the library in a single click, with the cell line, compound, dose range, and readout reagent editable to match the screens your lab actually runs.

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11. Conclusion

The ELabELN Cell Viability (MTS) Assay Experiment Template is not simply a digital version of a plate-reader export. It is a structured, audit-ready, searchable record that connects to your cell-line and reagent inventory, your SOPs and datasheets, the culture the screen followed, your plate reader and curve-fit tool, and the cytotoxicity-ranking, selectivity, and advancement workflows the viability value feeds — and, in the Suite edition, cross-plate cytotoxicity dashboards. It turns a viability screen into a record whose plate map, assay quality, and EC50 are captured, comparable, and defensible.

For a laboratory that runs viability screens regularly, the benefit compounds with every campaign. Plate maps, Z′-factors, and fit parameters accumulate into one queryable dose-response history. Every reagent and compound lot is traceable. Every screen is gated by its assay quality, and every advanced compound carries a defensible viability provenance — so a CC50 from a failing plate can no longer quietly drive a decision, and the dose-response trend that guides the campaign is built in rather than reconstructed.

The template is available to all ELabELN subscribers today. A new instance is live in one to two business days, and the first structured screen is typically documented within a week of account creation.

> **Get started**
> Visit elabeln.com/get-started to request your ELabELN instance, or contact LabLynx at 866.522.5969 or info@lablynx.com. Load the Cell Viability (MTS) template, configure it for your cell line and compound, and run your next screen from a tested, audit-ready baseline.

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